

Amendments to the claims

Claims 1-5, 7-15, and 25 are under examination.

Claim 7 is amended. Claims 8, 10-13, and 25 are cancelled.

The following list of claims will replace prior versions and listing of claims in the application:

1.(Original) A method of identifying the location of a mutation in the genome of a particular organism, said method comprising:

- a) isolating DNA from an organism having a mutated phenotype,
- b) contacting said DNA with a panel of restriction enzymes to produce several fragments of said DNA,
- c) introducing said fragments of DNA into a non-mutated host organism to transform said non-mutated organism into a mutated organism that expresses the mutated phenotype,
- d) determining the transformation frequency by counting number of the originally non-mutated host organisms of step (c) that express said mutated phenotype, and
- e) correlating said transformation frequency to the known locations of the restriction enzyme sites of step (b), to provide information regarding the location of said mutation in the genome.

2. (Original) The method of claim 1 wherein, the organism is selected from the group consisting of bacteria, fungi, yeast, Plasmodia and multicellular organisms.

3. (Original) The method of claim 2 wherein the bacteria is selected from the group consisting of bacteria for which the entire genomic DNA has been determined and bacteria for which the genomic DNA has been partially determined.

4. (Original) The method of claim 3 wherein the bacteria for which the entire genomic DNA has been determined is selected from the group consisting of:

Agrobacterium tumefaciens, *Caulobacter crescentus*, *Listeria monocytogenes*, *Borrelia burgdorferi*, *Brucella melitensis*, *Campylobacter jejuni*, *Clostridium perfringens*, *Corynebacterium glutamicum*, *Escherichia coli*, *Enterococcus faecalis*, *Helicobacter pylori*, *Mycoplasma pneumoniae*, *Mycoplasma genitalium*, *Pasteurella multocida*, *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas syringae*, *Rickettsia*

Synechococcus sp., *Toxoplasma gondii*, *Vibrio anguillarum*, *Vibrio sp.*, *Yersinia pseudotuberculosis*, *Yersinia enterocolitica* and, *Zymomonas mobilis*.

6. (Original) The method of claim 2, wherein the multicellular organism is mammalian.

7. (Currently Amended) The method of claim 1 wherein, the panel of restriction enzymes is selected from the group consisting of *AccI*, *AccII*, *AflIII*, *AluI*, *ApoI*, *AseI*, *BbvI*, *BfaI*, *BsaAI*, *BsaHI*, *BsaJI*, *BsrFI*, *BssKI*, *BstUI*, *BstYI*, *Cac8I*, *DdeI*, *DraI*, *FnuHI*, *FokI*, *HaeIII*, *HhaI*, *HinfI*, *HpaII*, *HphI*, *Hpy188I*, *Hpy99I*, *HpyCH4III*, *HpyCH4IV*, *HpyCH4V*, *MaeIII*, *MboII*, *MnII*, *MseI*, *MslI*, *NlaIII*, *NlaIV*, *RsaI*, *Sau3AI*, *Sau96I*, *SfaNI*, *SfcI*, *SmlI*, *SspI*, *TaqI*, *TfiI*, *TseI*, *Tsp45I*, *Tsp509I*, and *TspRI*.

8. (Cancelled)

9. (Original) The method of claim 1 wherein said transformation process of step (c) occurs by a process selected from the group comprising transduction and electroporation.

10. (Cancelled)

11. (Cancelled)

12. (Cancelled)

13. (Cancelled)

14. (Original) The method of claim 1 wherein, the correlation of said transformation frequency to the known locations of said restriction enzyme sites is obtained by a restriction map print out.

15. (Original) The method of claim 1 wherein, the correlation of said transformation frequency to the known locations of said restriction enzyme sites is obtained by a computerized program.

16. (Withdrawn) A method of identifying the precise locus and identity of a mutation in the genome of a particular organism, said method comprising:

- a) isolating DNA from an organism having a mutated phenotype,
- b) contacting said DNA with a panel of restriction enzymes to produce several fragments of said DNA,

c) introducing said fragments of DNA into a non-mutated host organism to transform said non-mutated organism into a mutated organism that expresses the mutated phenotype,

d) determining the transformation frequency by counting number of the originally non-mutated host organisms of step (c) that express said mutated phenotype,

e) correlating said transformation frequency to the known locations of the restriction enzyme sites of step (b), to provide information regarding the location of said mutation in the genome,

and further comprising,

f) amplifying candidate locations of said mutation in the genome by Polymerase Chain Reaction (PCR) using DNA from the mutant as template,

g) testing the amplified candidate locations for the ability to transform non-mutated host cells,

h) sequencing the amplified candidate location that transforms with high frequency, and

i) comparing the sequence of the amplification product to the sequence of the parent strain to precisely identify the locus and the identity of the mutation in the genome of a particular organism.

17. (Withdrawn) The method of claim 16 wherein, the organism is selected from the group consisting of bacteria, fungi, yeast, Plasmodia and multicellular organisms.

18. (Withdrawn) The method of claim 17 wherein the bacteria is selected from the group consisting of bacteria for which the entire genomic DNA has been determined and bacteria for which the genomic DNA has been partially determined.

19. (Withdrawn) The method of claim 17, wherein the multicellular organism is a mammalian.

20. (Withdrawn) The method of claim 16 wherein, the panel restriction enzymes is selected from the group consisting of *Acil*, *AclI*, *AflIII*, *AluI*, *ApoI*, *AseI*, *BbvI*, *BfaI*, *BsaAI*, *BsaHI*, *BsaJI*, *BsrFI*, *BssKI*, *BstUI*, *BstYI*, *Cac8I*, *DdeI*, *DraI*, *FnuII*, *FokI*, *HaeIII*, *HhaI*, *HinfI*, *HpaII*, *HphI*, *Hpy188I*, *Hpy99I*, *HpyCH4III*, *HpyCH4IV*, *HpyCH4V*, *MaeIII*, *MboII*, *MnII*, *MseI*, *MslI*, *NlaIII*, *NlaIV*, *RsaI*, *Sau3AI*, *Sau96I*, *SfaNI*, *SfcI*, *SmlI*, *SspI*, *TaqI*, *TfiI*, *TseI*, *Tsp45I*, *Tsp509I*, and *TspRI*.

21. (Withdrawn) The method of claim 16 wherein, the mutated phenotype is selected from the group consisting of drug resistance, increased production of proteins, increased ability to degrade waste and increased ability to detect analytes.

22. (Withdrawn) The method of claim 21 wherein the drug resistance is resistance to antibacterial agents.

23. (Withdrawn) A computerized method of identifying location of chromosomal mutations in the genome of a particular organism using a computer program, said method comprising:

- a) inputting enzyme transformation data into a computer, wherein said enzyme transformation data comprises the results of frequency of transformation of non-mutated host organism after introduction of DNA fragments from a mutated organism, wherein said DNA fragments have been digested by known restriction enzymes,
- b) inputting known map of restriction enzyme cleavage sites into said computer,
- c) inputting a group of variables that affect frequency of transformation into said computer,
- d) correlating inputs of steps (a), (b), and (c) to genome coordinate through said computer program, wherein said computer program scans genome sequence to identify locations of restriction enzyme cleavage sites in the genome that best fit the transformation frequency data, and
- e) comparing the transformation frequency data with the genome restriction enzyme cleavage map to identify the location of the mutation.

24. (Withdrawn) The method of claim 23 wherein the variables of step (c) comprise: (a) the distance of the mutation from the end of the DNA segment, (b) the length of the DNA segment and, and (c) in some species the presence of uptake signal sequences.

25. (Cancelled)